

FIG. 1A

1	AGACAGCGGA	ACTAAGAAA	GAGGCGCTGTGG	CACAGAA	CAATCATGTCTGACTCCCTG	60
	-----+	-----+	-----+	-----+	-----+	MetSerAspSerLeu
61	GTGGTGTGCGAGGTAGACCCAGAGCTAACAGAAA	GCTGAGGAAATTCGGCTTCCGAAAA	120			
	-----+	-----+	-----+			
	ValValCysGluValAspProGluLeuThrGluLysLeuArgLysPheArgPheArgLys					
121	GAGACAGACAATGCAGCCATCATATGAAGTGGACAAAGACCGCAGATGGTGGTGCTG	180				
	-----+	-----+				
	GluThrAspAsnAlaAlaIleIleMetLysValAspLysAspArgGlnMetValValLeu					
181	GAGGAAGAAATTCAGAACATTTCCCCAGAGGAGCTCAAAATGGAGTTGCCCGGAGAGACAG	240				
	-----+	-----+				
	GluGluGluPheGlnAsnIleSerProGluGluLeuLysMetGluLeuProGluArgGln					
241	CCCAGGTTTCGTGGTTTACAGCTACAAGTACGTGCATGACCATGGCCGAGTGTCCTACCCCT	300				
	-----+	-----+				
	ProArgPheValValTyrSerTyrLysTyrValHisAspAspGlyArgValSerTyrPro					

```

301  - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      LeuCysPheIlePheSerSerProValGlyCysLysProGluGlnGlnMetMetTyrAla
361  GGGAGTAAAAACAGGCTGGTGCAGACAGCAGAGCTCACAAAGGTGTTTCGAAATCCGCACC
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      GlySerLysAsnArgLeuValGlnThrAlaGluLeuThrLysValPheGluIleArgThr
421  ACTGATGACCTCACTGAGGCCCTGGCTCCCAAGAAAAGTTGTCTTTTCTTTCGTTGATCTCTG
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
      ThrAspAspLeuThrGluAlaTrpLeuGlnGluLysLeuSerPhePheArg
481  GGCTGGGGACTGAATTCCTGATGTCTGAGTCCTCAAGGTGACTGGGGACTTGGAACCCCT
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +
541  AGGACCTGAACAACCAAGACTTTAAATAAAATTTTAAATGCAAAAAATAAAAAAATAAAA
      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +

```

## FIG. 2

Query:	46	MSDSLVCVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVLVEEFFQNISPEELKME	225
		MS+SLVVC+V +L EKLKFRFRKET+NAAIIMK+DKD+++VVL+EE + ISP+ELK E	
Sbjct:	1	MSESLVVCDAEDLVEKLRKFRFRKETNNAAIIMKIDKDKRLVVLDEELEGISPDELKDE	60
Query:	226	LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV	405
		LPERQPRF+VYSYKY HDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKN+LVQTAELTKV	
Sbjct:	61	LPERQPRFIVYSYKYQHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNKLQTAELTKV	120
Query:	406	FEIRTTDDLTEAWLQEKLFFF	468
		FEIR T+DLTE WL+EKL FF	
Sbjct:	121	FEIRNTEDLTEEWLREKLGFF	141

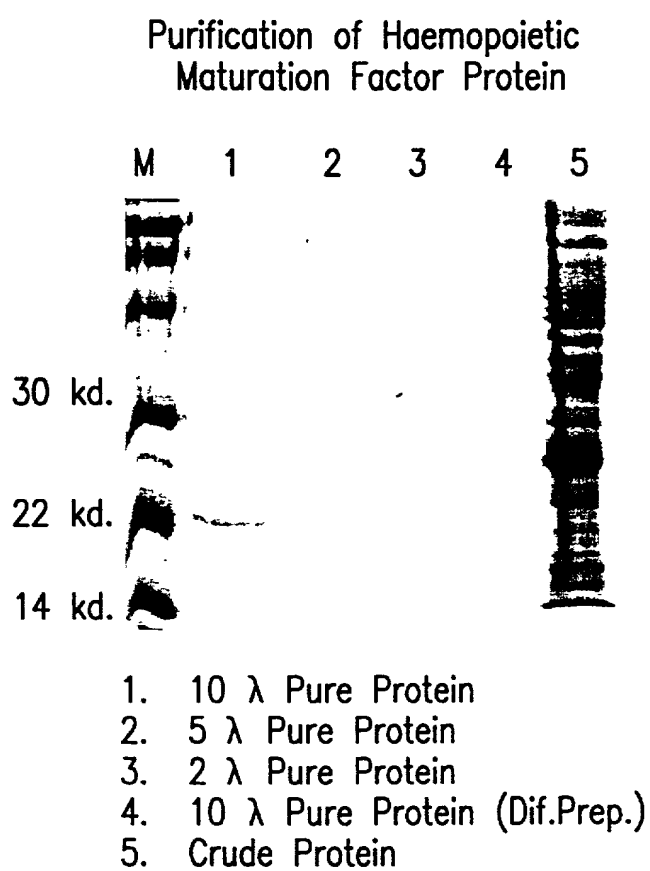


FIG.3

ANALYSIS OF THE HAEMOPOIETIC MATURATION FACTOR EXPRESSION MEDIA USING  
REVERSED-PHASE HPLC

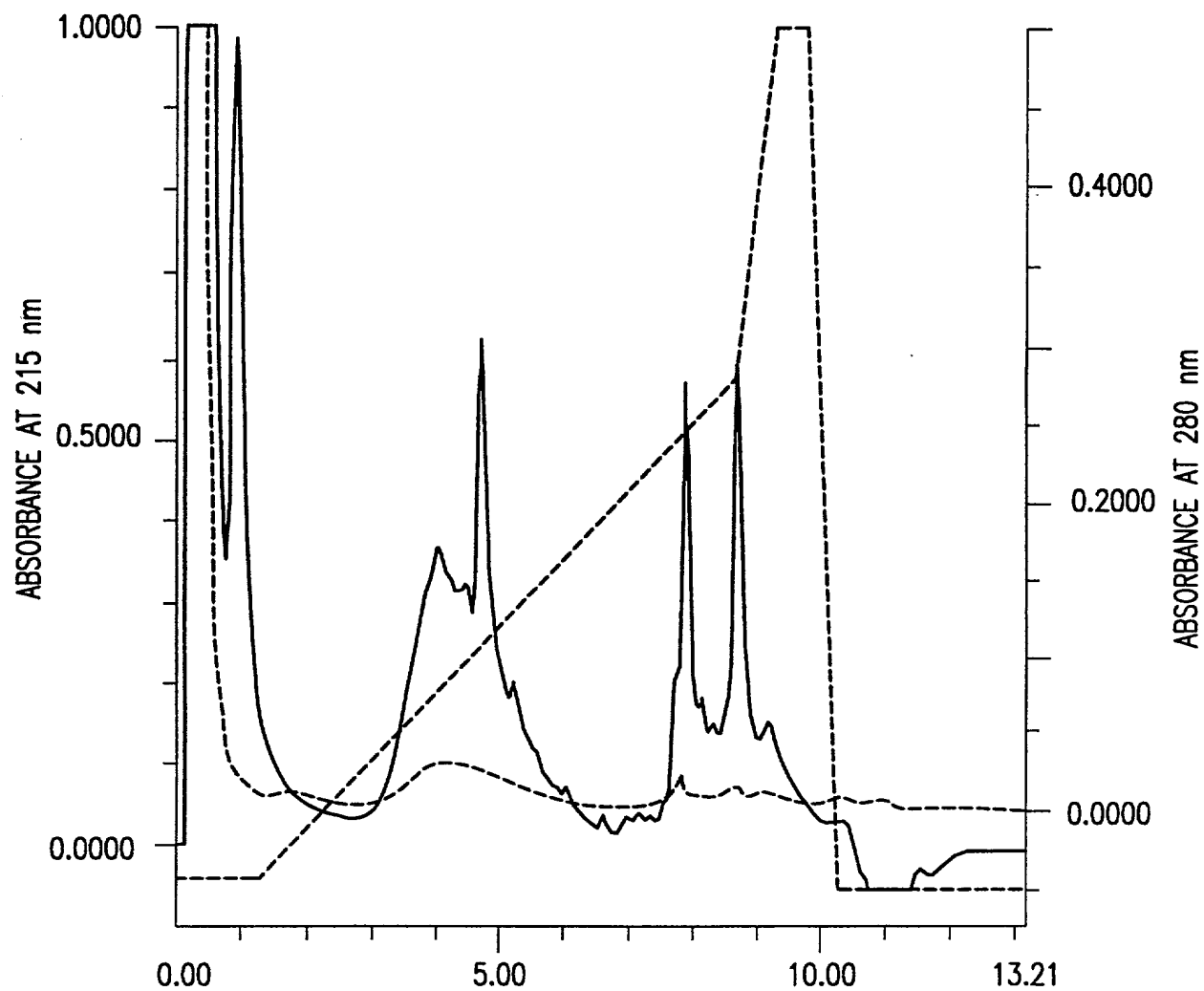


FIG.4A

ANALYSIS OF THE HAEMOPOIETIC MATURATION FACTOR EXPRESSION MEDIA BY  
REVERSED-PHASE HPLC AFTER PURIFICATION.

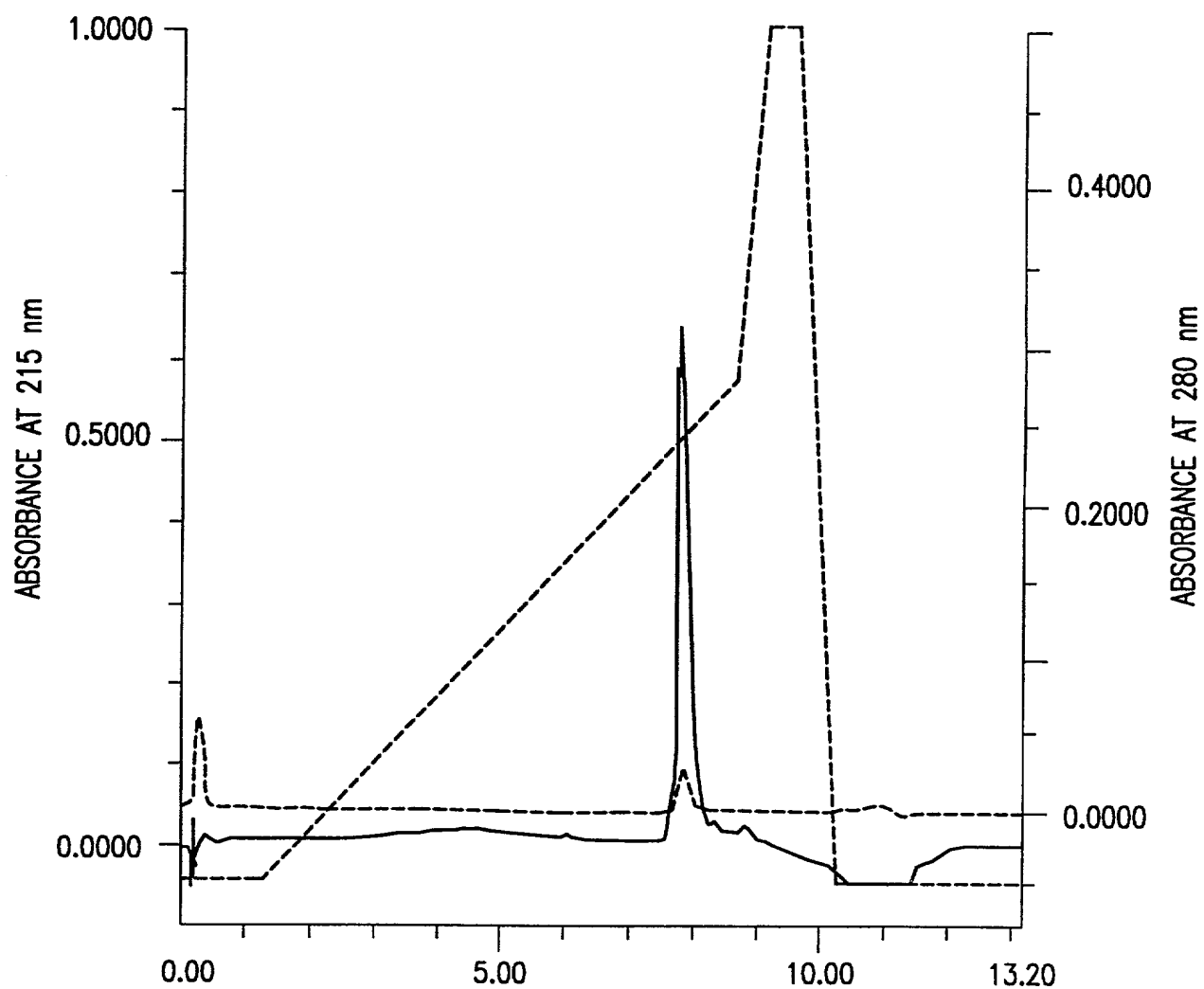


FIG.4B

QUANTIFICATION OF HUMAN MONOCYTE NORTHERN BLOT  
PROBED WITH HAEMOPOIETIC MATURATION FACTOR

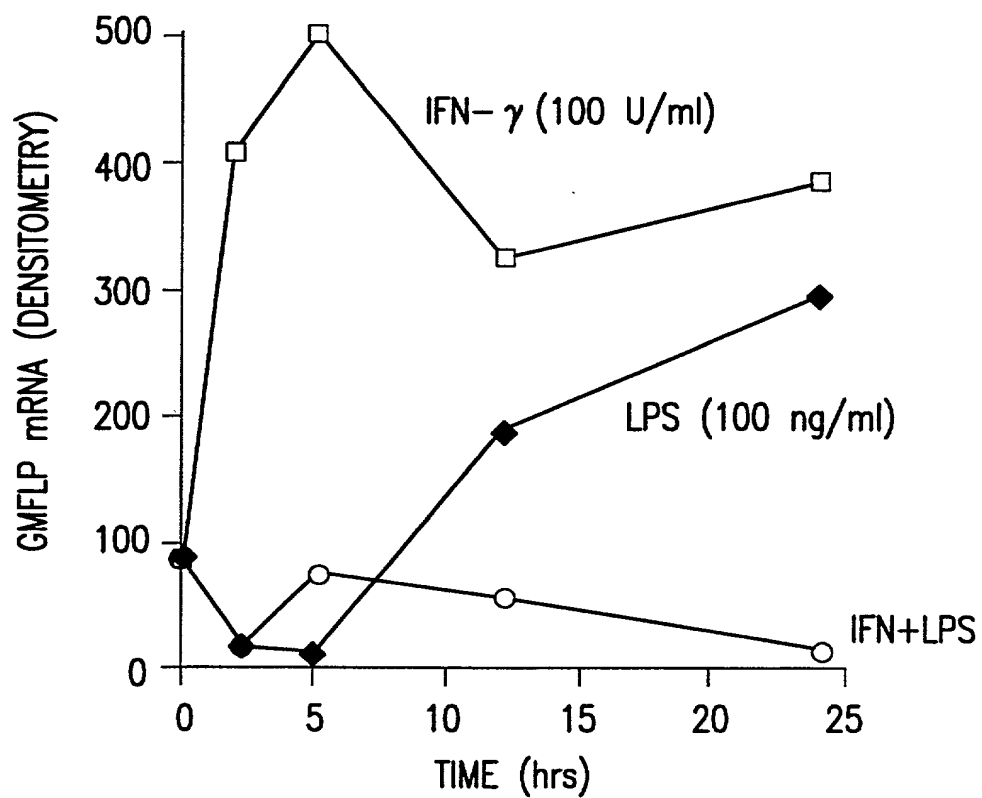


FIG.5

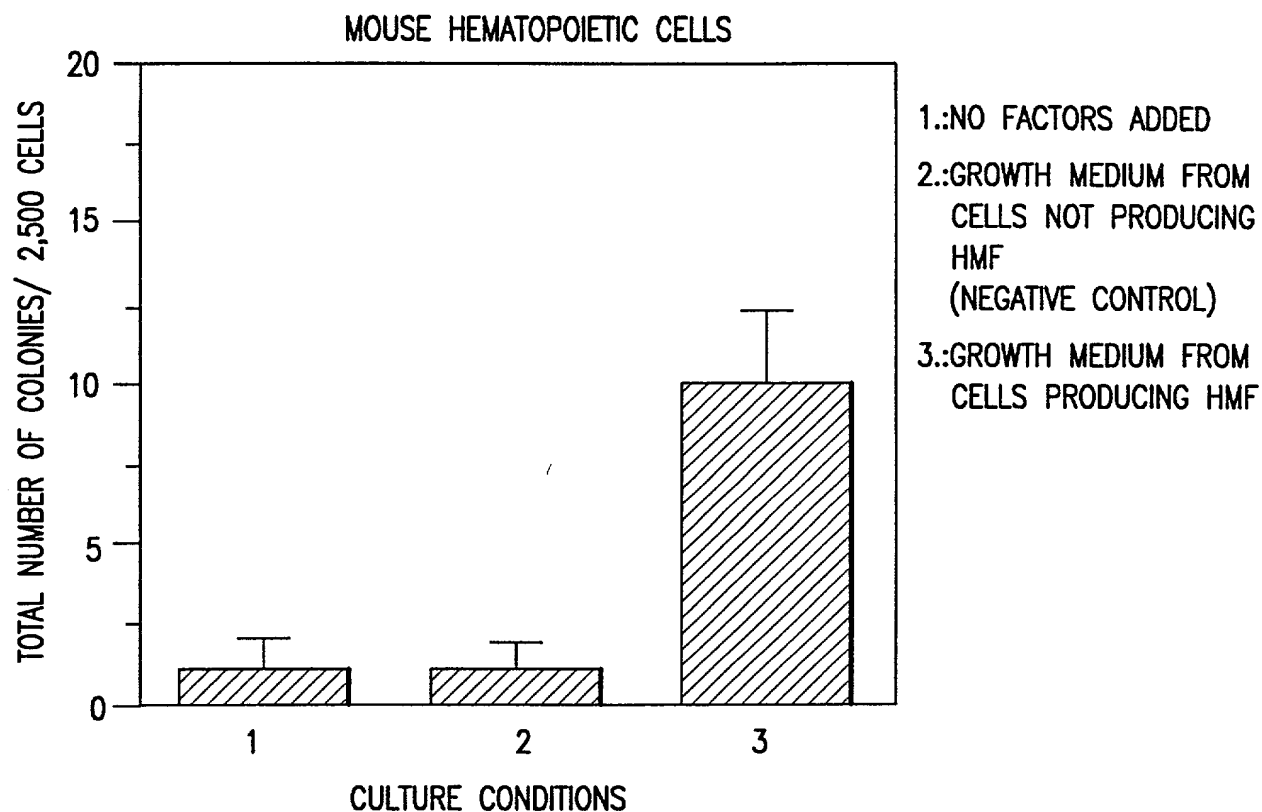


FIG.6A

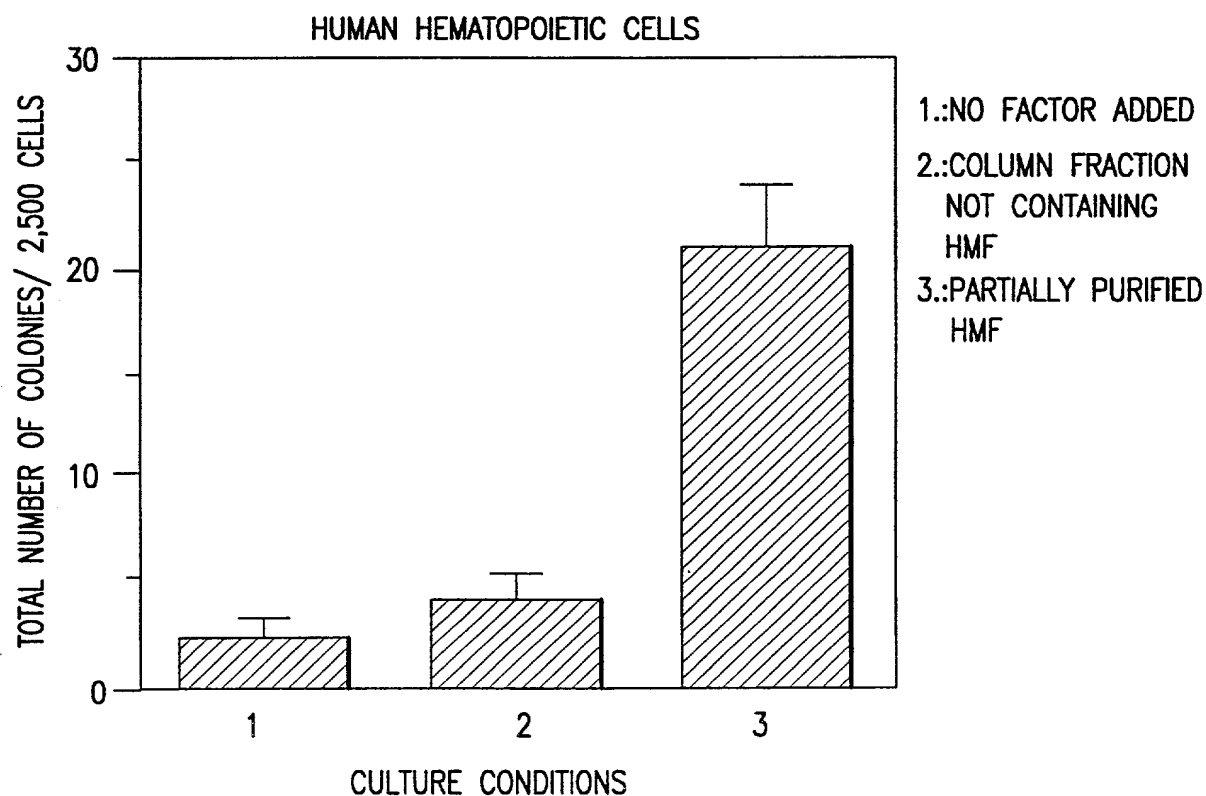


FIG.6B